

1 MSSKTA STNS IAQARRTVQQ LRLEASIERI KVS KASADLM SYCEEHARSD  
51 PLLMGIPTSE NPFKDKKTCI IL\*

51 PLLMG IPTSE NPFKDKKTCI IL\*

**Figure 2:** cDNA sequence of mGy12 variant 1 (SEQ ID NO:2)

1 CTAGAATTCA GCGGCCGCTG AATTCTAGGC GACGACGGCG AAGAGTGAGT  
51 GCCAAGGTTC ATATGGGAAG GACTTTGGGG TGAGCATCTT CTCTATTTCC  
101 AGCTGGCTTT TCTGATTTTC AGAAAGAAGA CTCATCAAAG ATGTCCAGCA  
151 AGACGGCAAG CACCAACAGC ATAGCCCAAG CCAGGAGAAC TGTGCAGCAG  
201 CTGAGATTGG AAGCCTCCAT CGAAAGAATA AAGGTCTCAA AAGCATCAGC  
251 AGACCTGATG TCATACTGTG AGGAGCATGC CCGGAGCGAC CCCCTGCTGA  
301 TGGGCATACC GACCTCAGAA AACCCGTTCA AGGATAAGAA GACCTGCATC  
351 ATCTTATAGT GGACCAGGAA GCGCCCCTTG CCTCTTAACG CAAACCACAG  
401 CAGCAACCTG AAGGGATTCC TTCAGCTTAC CTGGTAACCA CAGCTAGTAA  
451 CTAAACACC CTTCTCTCGG AATAATAGAC CCTGAAGTCT CTCTTTTTCA  
501 AGTTGTCCTT TCTTCACCCT TTACTGATTT AATACAGAAT AACAATCTTA  
551 TTTTCTATTT GATAACTATG GTATCATATT GGGTTACTGT ATAAGGAAAA  
601 TGGCAGGGGA GTTGTGGGAA GCTTGTCTTT ACAAATATA ATTGATTAAG  
651 ATATGTCAAG ACCTACATTG TCTAAGCACC GGCAAATTAA AATGTCGAGA  
701 ATCACTTCAG TCAAAAACCT TTATATTCTG TTCTTAATAA TGTTTGTGCC  
751 AACCTATATC CCATGTAAGG GATCTGGGGA GGAGGCATGT GTCTACAACC  
801 ATACCTTTTT GCACTATGGG CACTAACCAC CCTGAACTT CCTGCGGTAG  
851 CTCCCTCCCT TCAGAGTTAC ATCATTATCC TGA CTCTGTG TAGGTAAATT  
901 TCCGTGAAAT TTTTGTACAA AAAAAAGGTA ATGAAAGAAC GTTGCAAAGA  
951 TCATCTGCAT TATAATGAGT TGATGCTGTT CTCCTCCTC TCTTGGAATT  
1001 GTGCTGGCCC CTTAGTCTAC AATAAACTGT GCCAATTAAA AACCTAAGGC  
1051 TAAAACTGAA AGCCCTTTGA TGGGGTCTTA ACTCATATCA GTCATTTGGG  
1101 CTTCTCTGAT CCTGAGGCTA AGAAAGGGGA AGAGACCCTC AGGAGGCAGC  
1151 TTCCACTCCA GGGCTCTTGA TCTCTGCTGG ATTGGGGGTG GCCACCTCAG  
1201 AACTTCCAC CCTCATGACT GGAATGGAAG AGGGGACCGA GAGCCTCACA

1251 ATCTCGGAGA GGGAGGAGAA ATTCTTAAAA ACAGCTGCTC TCCTGCGCCC  
 1301 AGCTTCACAG GCAGCCCTGC CCCTTTCTCC TCACCAGCAT GGTACCTGCC  
 1351 CTTACTGCTA GAGCAGCTGC TTGTAGAGGG ACATTCCCTC CTTCCCAGTT  
 1401 TTAAGTGGTG GACCACAGTG GGGGGAAAAA CATTCAAGCG ATATAAAGAC  
 1451 ACTTGGGCTC TTTGCAGATG CCTATACTTC CAACACTACC ATGTCCACAA  
 1501 ACCACCCTGG GGGAGGGCCC TTCCAAAGGG AGGCTTGCTA GTTTCAGCGT  
 1551 CTAGCAGTTG GGTCCTCACT TTTACTCCAA TTGTGAAAAT AGCCCCACGTA  
 1601 CCCTCGCAGT GTCCAGTAGG GATCCCAGAG GCACATAACC AAGAAAGGAT  
 1651 TTTGACTTTG TCACAGTGAC TATTTAAAAA AATCTATTCG AAGTCCAAAC  
 1701 CAAACACAAA GCCTGTGATA TTTTAGGTTA TTAAGGTAAC TGCTAATGAA  
 1751 GGATTTTAAA AAGTGTCTCT AAAAAGGACT TAGCCCCGGG AGTTGTTTAT  
 1801 AAAATTTCCC CCACTTGTAT ACAGTGTGCA CTAAAAGAAA ATGTATTTTA  
 1851 ATATCTAATG CCTGGGCTCT GAGCGTCATG CTTCTTGGTG GTAAACATGC  
 1901 AGTCCTGTTC CTAAGTGACT CAGAGGCATC AGAATTTCTC CACGTTACCC  
 1951 ATCTGCTTGG CACTCGGAAC TGAGCGTGTG AAATCCATAG CGCTGCCCAC  
 2001 AACCTGTTCT CACTGCTTAG CTCCCAGCTG GATTAAAGAC ACCTGCTCAG  
 2051 GCGGGAGAGA GAGAGAGAGA GCGAGCTTTT ACCTTGAAA AGGTAAAGAT  
 2101 GGAAATGTAC ACCAAAAAAG ACAATTTTTA CATTTAATGG AACATTCTTT  
 2151 TTTTTTACAA GTATATTTTT CTACTGATAG TTTCAGAACA CTAATCTTAT  
 2201 ATTCACTCTA ATCTTAAACA TGTTTCTTTA AATATTTATA AGGCAGTTTA  
 2251 TTACAGAATA TTTTCATGCA ATCATGTGCA CATTATTGGT AGCAAACATA  
 2301 GTATATCCTT TAGTACTTTA GCATATTTTT GTTAAAATAC TTTTAATGGT  
 2351 AAGAAATGAA CTTGAGGTCC CAGGAGGTTT TGTTGCCTTT TCATTGATTA  
 2401 GAGACAATAA ATATCTTGTA ACTTCCTAAC CAGATCTGAG CTGTGCTCAC  
 2451 AATAATAATA ATGAAATCAG ATTCTTTGAT GCTGGACTCA GGAGGGAAAT

2501 CATTAGCCAA CTGTTGACTT ACTTATAGCT AGATGTCTAT GTGAGAAAGT  
2551 ATAATATATA TATATACACA TATATATGAC ATGTAAGAGT CACTTTTATT  
2601 TATCTGTCTT TGTTCACTTA TGAAGCCGGT AACTGCAGCA GTATGTTGGT  
2651 GATGTCATGA TGCACAGAAG TCCCATGTGG AGTGTTTTTC CCACACTGAC  
2701 AACTTGGCCT CCTTTCTGTG TGTTCACTCT GTTGTCTGAA CTAACACTCC  
2751 CGCGAGCACT ATACTCTTTA TACTCTGATC CCCCTAGTTC ATCTTAAATT  
2801 TGTCTGTGGC CCTGGCAAGA TAGCGTACAC AAGATTCCAT GACTCCAGAG  
2851 CATCTTGAAG AAACATACAT ATTTTGAAAG AGGGGAAATG TAGCAGATAG  
2901 TTCACAAGCT GCGGGTTGTA GCTAAATATT CCATTTCTTT GAAATCATGT  
2951 TTCTAAATTC TTTACCATCA GAAAGAAAAG GAGTGTCTATA CACTTTCAAG  
3001 GGAAGGCTTG GTCTGCGTTT TCTGTGTTTG GATTATTTTT ATACTTTGCT  
3051 GATCTTTAAG CTATCCATGG GGGAAATTTT ATACCAACGA GTTAATAATT  
3101 CTCATTCATC GTTTACACAA TGTAACATGT GTCATACTGG GGCCAGCGAG  
3151 ATGGCTCAGT AGGTAAAGGT GCTTGATGCT AAGCCCGGCA GCCTGTGTTT  
3201 CATCTACAGG ATGCACAACA TAAAAGAAAA GATCTGATTC CCACAGGTTC  
3251 TCTTCTGACC TACACACACA CACACTAAAA TAACATTTAA AAATATGTGC  
3301 CAAATTATAT TTGTTTCGGGT GCCACCTTCC ACCAGCTTAC CACTACGGTA  
3351 GAACTGTCAA ATTCATCTCC CTGAATTTGT CTTAAAGGGG TGTCCATGCA  
3401 CAGGCCCAAG AGTCACCTCC AATGAAATAA ATGTAATACT GAAGTATGCC  
3451 ATGATGTTTG TTGTTTTCTT TCATCGTAAG CCTGTAAGCA GGAAAAATAC  
3501 GTCAAATCAG ATAGAATAGA GCATTTACCA GTGGTCGATG GCCTGGTCAG  
3551 TCCTGTGCCG GGTGACTTAG GACCAGGCAC GTCAGCTCTC TGAGCCTCCC  
3601 CTTCCCTTGT TGTCACAAGG GAATAGAAGC AGAAGAAGCT GAGAGCCTCC  
3651 CTATTCCCAG ATGCCCTGGT GGAATGACCT GCCTCTCTGC CGTTTCTGCC  
3701 AACGTGTTGG TGCTATAAGC TGCTTCAAAT ACCAGTTTGT CTGTAGTGTG  
3751 TACTCACCTA ATCACTTGTT ATCCAGTGCC TGTCTAGGT TTATGGACTT



**Figure 3:** cDNA sequence of mGy12 variant 2 (SEQ ID NO:3)

1 GCAGCGGCGG CGGCGGCGAC GACGGCGAAG AGTTCATATG GGAAGGACTT  
51 TGGGGTGAGC ATCTTCTCTA TTTCCAGCTG GCTTTTCTGA TTCACCCAC  
101 CATTTAAAAC CTGGAGGCAC TGGGCCACAC AAAGCCTTGC TGATTTTCAG  
151 AAAGAAGACT CATCAAAGAT GTCCAGCAAG ACGGCAAGCA CCAACAGCAT  
201 AGCCCAAGCC AGGAGAACTG TGCAGCAGCT GAGATTGGAA GCCTCCATCG  
251 AAAGAATAAA GGTCTCAAAA GCATCAGCAG ACCTGATGTC ATACTGTGAG  
301 GAGCATGCCC GGAGCGACCC CCTGCTGATG GGCATACCGA CCTCAGAAAA  
351 CCCGTTCAAG GATAAGAAGA CCTGCATCAT CTTATAGTGG ACCAGGAAGC  
401 GCCCCTTGCC TCTTAACGCA AACCACAGCA GCAACCTGAA GGGATTCCCTT  
451 CAGCTTACCT GGTAACCACA GCTAGTAACT AAAACACCCT TCTCTCGGAA  
501 TAATAGACCC TGAAGTCTCT CTTTTTCAAG TTGTCCTTTC TTCACCCTTT  
551 ACTGATTTAA TACAGAATAA CAATCTTATT TTCTATTTGA TAACTATGGT  
601 ATCATATTGG GTTACTGTAT AAGGAAAATG GCAGGGGAGT TGTGGGAAGC  
651 TTGTCTTTAC AAAATATAAT TGATTAAGAT ATGTCAAGAC CTACATTGTC  
701 TAAGCACCGG CAAATTAAAA TGTCGAGAAT CACTTCAGTC AAAAACCTTT  
751 ATATTCTGTT CTTAATAATG TTTGTGCCAA CCTATATCCC ATGTAAGGGA  
801 TCTGGGGAGG AGGCATGTGT CTACAACCAT ACCTTTTTGC ACTATGGGCA  
851 CTAACCACCC TGAAACTTCC TGCGGTAGCT CCCTCCCTTC AGAGTTACAT  
901 CATTATCCTG ACTCTGTGTA GGTAAATTTC CGTGAAATTT TTGTACAAAA  
951 AAAAGGTAAT GAAAGAACGT TGCAAAGATC ATCTGCATTA TAATGAGTTG  
1001 ATGCTGTTCT CACTCCTCTC TTGGAATTGT GCTGGCCCCT TAGTCTACAA  
1051 TAAACTGTGC CAATTAAAAA CCTAAGGCTA AACTGAAAG CCCTTTGATG  
1101 GGGTCTTAAC TCATATCAGT CATTTGGGCT TCTCTGATCC TGAGGCTAAG  
1151 AAAGGGGAAG AGACCCTCAG GAGGCAGCTT CCACTCCAGG GCTCTTGATC

1201 TCTGCTGGAT TGGGGGTGGC CACCTCAGAA ACTTCCACCC TCATGACTGG  
1251 AATGGAAGAG GGGACCGAGA GCCTCACAAT CTCGGAGAGG GAGGAGAAAT  
1301 TCTTAAAAAC AGCTGCTCTC CTGCGCCCAG CTTACAGGC AGCCCTGCCC  
1351 CTTTCTCCTC ACCAGCATGG TACCTGCCCT TACTGCTAGA GCAGCTGCTT  
1401 GTAGAGGGAC ATTCCCTCCT TCCCAGTTTT AACTGGTGGA CCACAGTGGG  
1451 GGGAAAAACA TTCAAGCGAT ATAAAGACAC TTGGGCTCTT TGCAGATGCC  
1501 TATACTTCCA ACACTACCAT GTCCACAAAC CACCCTGGGG GAGGGCCCTT  
1551 CCAAAGGGAG GCTTGCTAGT TTCAGCGTCT AGCAGTTGGG TCCTCACTTT  
1601 TACTCCAATT GTGAAAATAG CCCACGTACC CTCGCAGTGT CCAGTAGGGA  
1651 TCCCAGAGGC ACATAACCAA GAAAGGATTT TGACTTTGTC ACAGTGAATA  
1701 TTTAAAATAA TCTATTCGAA GTCCAAACCA AACACAAAGC CTGTGATATT  
1751 TTAGGTTATT AAGGTAAGT CTAATGAAGG ATTTTAAAAA GTGTCCTCAA  
1801 AAAGGACTTA GCCCCGGGAG TTGTTTATAA AATTTCCCCC ACTTGTATAC  
1851 AGTGTGCACT AAAAGAAAAT GTATTTTAAT ATCTAATGCC TGGGCTCTGA  
1901 GCGTCATGCT TCTTGGTGGT AAACATGCAG TCCTGTTTCT AAGTGAATCA  
1951 GAGGCATCAG AATTTCTCCA CGTTACCCAT CTGCTTGGCA CTCGGAAGTG  
2001 AGCGTGTGAA ATCCATAGCG CTGCCCACAA CCTGTTCTCA CTGCTTAGCT  
2051 CCCAGCTGGA TTAAAGACAC CTGCTCAGGC GGGAGAGAGA GAGAGAGAGC  
2101 GAGCTTTTAC CTTGGAAAAG GTAAAGATGG AAATGTACAC CAAAAAAGAC  
2151 AATTTTTTACA TTTAATGGAA CATTCTTTTT TTTTACAAGT ATATTTTTCT  
2201 ACTGATAGTT TCAGAACACT AATCTTATAT TCACTCTAAT CTTAAACATG  
2251 TTTCTTTAAA TATTTATAAG GCAGTTTATT ACAGAATATT TTCATGCAAT  
2301 CATGTGCACA TTATTGGTAG CAAACATAGT ATATCCTTTA GTACTTTAGC  
2351 ATATTTTTGT TAAAATACTT TTAATGGTAA GAAATGAACT TGAGGTCCCA  
2401 GGAGGTTTTG TTGCCTTTTC ATTGATTAGA GACAATAAAT ATCTTGTAAC

2451 TTCCTAACCA GATCTGAGCT GTGCTCACAA TAATAATAAT GAAATCAGAT  
 2501 TCTTTGATGC TGGACTCAGG AGGGAAATCA TTAGCCAACT GTTGACTIONAC  
 2551 TTATAGCTAG ATGTCTATGT GAGAAAGTAT AATATATATA TATACACATA  
 2601 TATATGACAT GTAAGAGTCA CTTTTATTTA TCTGTCTTTG TTCACTTATG  
 2651 AAGCCGGTAA CTGCAGCAGT ATGTTGGTGA TGTCATGATG CACAGAAGTC  
 2701 CCATGTGGAG TGTTTTTCCC AACTGACAA CTTGGCCTCC TTTCTGTGTG  
 2751 TTCAGTCTGT TGTCTGAACT AACACTCCCC CGAGCACTAT ACTCTTTATA  
 2801 CTCTGATCCC CCTAGTTCAT CTTAAATTTG TCTGTGGCCC TGGCAAGATA  
 2851 GCGTACACAA GATTCCATGA CTCCAGAGCA TCTTGAAGAA ACATACATAT  
 2901 TTTGAAAGAG GGGAAATGTA GCAGATAGTT CACAAGCTGC GGGTTGTAGC  
 2951 TAAATATTCC ATTTCTTTGA AATCATGTTT CTAAATTCTT TACCATCAGA  
 3001 AAGAAAAGGA GTGTCATACA CTTTCAAGGG AAGGCTTGGT CTGCGTTTTTC  
 3051 TGTGTTTGGA TTATTTTTAT ACTTTGCTGA TCTTTAAGCT ATCCATGGGG  
 3101 GAAATTTTAT ACCAACGAGT TAATAATTCT CATTCACTGT TTACACAATG  
 3151 TAACATGTGT CATACTGGGG CCAGCGAGAT GGCTCAGTAG GTAAAGGTGC  
 3201 TTGATGCTAA GCCCGGCAGC CTGTGTTTCA TCTACAGGAT GCACAACATA  
 3251 AAAGAAAAGA TCTGATTCCC ACAGGTTCTC TTCTGACCTA CACACACACA  
 3301 CACTAAAATA ACATTTAAAA ATATGTGCCA AATTATATTT GTTCGGGTGC  
 3351 CACCTTCCAC CAGCTTACCA CTACGGTAGA ACTGTCAAAT TCATCTCCCT  
 3401 GAATTTGTCT TAAAGGGGTG TCCATGCACA GGCCCAAGAG TCACCTCCAA  
 3451 TGAAATAAAT GTAATACTGA AGTATGCCAT GATGTTTGTT GTTTTCTTTC  
 3501 ATCGTAAGCC TGTAAGCAGG AAAAATACGT CAAATCAGAT AGAATAGAGC  
 3551 ATTTACCAGT GGTCGATGGC CTGGTCAGTC CTGTGCCGGG TGACTIONAGGA  
 3601 CCAGGCACGT CAGCTCTCTG AGCCTCCCCT TCCCTTGTTG TCACAAGGGA  
 3651 ATAGAAGCAG AAGAAGCTGA GAGCCTCCCT ATTCCCAGAT GCCCTGGTGG  
 3701 AATGACCTGC CTCTCTGCCG TTTCTGCCAA CGTGTTGGTG CTATAAGCTG



3751 CTTCAAATAC CAGTTTGTCT GTAGTGTGTA CTCACCTAAT CACTTGTTAT  
3801 CCAGTGCCTG TTCTAGGTTT ATGGACTTAA CTATTTCTGT GATGTTTCAT  
3851 TTTTAGCCAT GTTAACTCCT AACACATATT CTCTTATGTC TCAGTAAAGT  
3901 TTCATTTGAT AAGTTGTTGA GATTCTGTGA TTTGATAATA TTCTTCGGCT  
3951 GTCCATCCAG CATCTTAATC ACTTTAAAAC TGTGATTGTT ATTTGCAACT  
4001 CTGTTCTTTG GAAAGAATAA AAGCATTTTT TTTCACTTGC TAACATGCTC  
4051 ACAAATGTGA GAGAAGAGTC ATTAAAAGCT TTACTTACTG GGTCAGTGCG  
4101 TCATTGACTC CTTTCTGTGT TTTGCCCAAT AAATTAATAA AAGACCAAAA  
4151 AAAAAAAAAA AAAAAAAAAA AAAAA

1. MSSKTASTNN IAQARRTVQQ LRLEASIERI KVS KASADLM SYCEEHARSD  
51. PLLIGIPTSE NPFKDKKTCI IL

1. MSSKTASTNN IAQARRTVQQ LRLEASIERI KVSASADLM SYCEEHARSD  
51. PLLIGIPTSE NPFKDKKTCI IL

1000 900 800 700 600 500 400 300 200 100 0



FIGURE 5